

SEQUENCE LISTING

<110> Chadwick, Brian Paul
Frischauf, Anna-Maria

<120> METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
POLYPEPTIDES AND NUCLEIC ACIDS

<130> 9598-066

<140> 09/240,639
<141> 1999-01-29

<160> 29

<170> PatentIn Ver. 2.0

<210> 1
<211> 2762

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232)..(1599)

<400> 1
gtggggtcgt atcccgccgg tggaggccgg ggtggcgccg gccggggccgg gggagccaa 60
aagaccggct gccgcctgct ccccgaaaaa gggcactcgt ctccgtgggt gtggcggagc 120
gcgcgggtgca tggaatgggc tatgtgaatg aaaaaaggtt tccgttatga aacttccaga 180
aaaacgagct acatttttca gcagccgcag cacggtcctt ggcaaacaag g atg aga 237
Met Arg
1

aaa ata tcc aac cac ggg agc ctg cgg gtg gcg aag gtg gca tac ccc 285
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
5 10 15

ctg ggg ctg tgt gtg ggc gtg ttc atc tat gtt gcc tac atc aag tgg 333
Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
20 25 30

cac cgg gcc acc gcc acc cag gcc ttc ttc agc atc acc agg gca gcc 381
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
35 40 45 50

ccg ggg gcc cgg tgg ggt cag cag gcc cac agc ccc ctg ggg aca gct 429
Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala
55 60 65

gca gac ggg cac gag gtc ttc tac ggg atc atg ttt gat gca gga agc 477
Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser
70 75 80

act ggc acc cga gta cac gtc ttc cag ttc acc cgg ccc ccc aga gaa	525
Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu	
85 90 95	
act ccc acg tta acc cac gaa acc ttc aaa gca gtg aag cca ggt ctt	573
Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu	
100 105 110	
tct gcc tat gct gat gat gtt gaa aag agc gct cag gga atc cgg gaa	621
Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu	
115 120 125 130	
cta ctg gat gtt gct aaa cag gac att ccg ttc gac ttc tgg aag gcc	669
Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala	
135 140 145	
acc cct ctg gtc ctc aag gcc aca gct ggc tta cgc ctg tta cct gga	717
Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly	
150 155 160	
gaa aag gcc cag aag tta ctg cag aag gtg aaa gaa gta ttt aaa gca	765
Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala	
165 170 175	
tcg cct ttc ctt gta ggg gat gac tgt gtt tcc atc atg aac gga aca	813
Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr	
180 185 190	
gat gaa ggc gtt tcg gcg tgg atc acc atc aac ttc ctg aca ggc agc	861
Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser	
195 200 205 210	
ttg aaa act cca gga ggg agc agc gtg ggc atg ctg gac ttg ggc gga	909
Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly	
215 220 225	
gga tcc act cag atc gcc ttc ctg cca cgc gtg gag ggc acc ctg cag	957
Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln	
230 235 240	
gcc tcc cca ccc ggc tac ctg acg gca ctg cgg atg ttt aac agg acc	1005
Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr	
245 250 255	
tac aag ctc tat tcc tac agc tac ctc ggg ctc ggg ctg atg tcg gca	1053
Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala	
260 265 270	
cgc ctg gcg atc ctg ggc ggc gtg gag ggg cag cct gct aag gat gga	1101
Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly	
275 280 285 290	
aag gag ttg gtc agc cct tgc ttg tct ccc agt ttc aaa gga gag tgg	1149
Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp	
295 300 305	

gaa cac gca gaa gtc acg tac agg gtt tca ggg cag aaa gca gcg gca Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala 310	315	320	1197	
agc ctg cac gag ctg tgt gct gcc aga gtg tca gag gtc ctt caa aac Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn 325	330	335	1245	
aga gtg cac agg acq gag gaa gtg aag cat gtg gac ttc tat gct ttc Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe 340	345	350	1293	
tcc tac tat tac gac ctt gca gct ggt gtg ggc ctc ata gat gcg gag Ser Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu 355	360	365	370	1341
aag gga ggc agc ctg gtg gtg ggg gac ttc gag atc gca gcc aag tac Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr 375	380	385	1389	
gtg tgt cgg acc ctg gag aca cag ccg cag agc agc ccc ttc tca tgc Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys 390	395	400	1437	
atg gac ctc acc tac gtc agc ctg cta ctc cag gag ttc ggc ttt ccc Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro 405	410	415	1485	
agg agc aaa gtg ctg aag ctc act cgg aaa att gac aat gtt gag acc Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr 420	425	430	1533	
agc tgg gct ctg ggg gcc att ttt cat tac atc gac tcc ctg aac aga Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg 435	440	445	450	1581
cag aag agt cca gcc tca tagtggccga gccatccctg tccccgtcag Gln Lys Ser Pro Ala Ser 455				1629
cagtgtctgt gtgtctgcat aaaccctcct gtcctggacg tgacttcatc ctgaggagcc 1689				
acagcacagg ccgtgctggc actttctgca cactggctct gggacttgca gaaggcctgg 1749				
tgctgccctg gcatcagcct cttccagtc catctggcca gagggctgtc tggacctggg 1809				
ccctgctcaa tgccacctgt ctgcctgggc tccaaagtggg caggaccagg acagaaccac 1869				
aggcacacac tgagggggca gtgtggctcc ctgcctgtcc catccccatg ccccgccgc 1929				
ggggctgtgg ctgctgctgt gcatgtccct gcgatggag tcttgcgtcc cagcctgtca 1989				
gtttcctccc cagggcagag ctccccctcc tgcataagatc tgggaggcgg tgcaggctgt 2049				
cctggctgct ctggggaaagc cgagggacag ccataacacc cccgggacag taggtctggg 2109				
cggcaccact ggaaactctg gacttgagtg tggttgcgtct tccttgggta tgaatgtgtg 2169				

agttcaccca gaggcctgct ctcctcacac attgtgtggt ttggggtaa tcatggagg 2229
agacacacctt tcatagacgg caggtgccc ccttcaggg agtctccag catgggcgga 2289
tgccgggcat gagctgtgt aaactatgg tggctgtgct gctttagtga cgtctctgtc 2349
gtgtgggtgc caagtgtttg tgttagaaact gtgttcttag ccccttttc tggacaccaa 2409
ctgtgtctg tgaatgtatc gctactgtga gctgttcccg cctagccagg gccatgtctt 2469
aggtgcagct gtgccacggg tcagctgagc cacagtccca gaaccaagct ctcgggtct 2529
cgggcccacca tccgcccacc tcgggctgac cccacccctt ccatggacag tggagcccc 2589
ggccgtgca tcctgctcag tgtggcgtca gtgtggggc tgagccctt gagctgcttc 2649
agtgaatgtc cagtgcccg cacgagctga acctcatgtg ttccactccc aataaaaggt 2709
tgacaggggc ttctccttca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2762

<210> 2
<211> 456
<212> PRT
<213> Homo sapiens

<400> 2
Met Arg Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala
1 5 10 15
Tyr Pro Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile
20 25 30
Lys Trp His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg
35 40 45
Ala Ala Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly
50 55 60
Thr Ala Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala
65 70 75 80
Gly Ser Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro
85 90 95
Arg Glu Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro
100 105 110
Gly Leu Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile
115 120 125
Arg Glu Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp
130 135 140
Lys Ala Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu
145 150 155 160

Pro Gly Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe
165 170 175

Lys Ala Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn
180 185 190

Gly Thr Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr
195 200 205

Gly Ser Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu
210 215 220

Gly Gly Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr
225 230 235 240

Leu Gln Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn
245 250 255

Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met
260 265 270

Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys
275 280 285

Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly
290 295 300

Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala
305 310 315 320

Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu
325 330 335

Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr
340 345 350

Ala Phe Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp
355 360 365

Ala Glu Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala
370 375 380

Lys Tyr Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe
385 390 395 400

Ser Cys Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly
405 410 415

Phe Pro Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val
420 425 430

Glu Thr Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu
435 440 445

Asn Arg Gln Lys Ser Pro Ala Ser
450 455

```

<210> 3
<211> 2797
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (83)...(1669)

<400> 3
acccacgcgt ctggccgcgg gccgcctctg cggcagcgct agtcgccttc tccgaatcg 60
ctccgcacag ctaggagaaa ag atg ttc act gtg ctg acc cgc caa cca tgt 112
                           Met Phe Thr Val Leu Thr Arg Gln Pro Cys
                           1           5           10

gag caa gca ggc ctc aag gcc ctc tac cga act cca acc atc att gcc 160
Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala
                           15          20          25

ttg gtg gtc ttg ctt gtg agt att gtg gta ctt gtg agt atc act gtc 208
Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val
                           30          35          40

atc cag atc cac aag caa gag gtc ctc cct cca gga ctg aag tat ggt 256
Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly
                           45          50          55

att gtg ctg gat gcc ggg tct tca aga acc aca gtc tac gtg tat caa 304
Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln
                           60          65          70

tgg cca gca gaa aaa gag aat aat acc gga gtg gtc agt caa acc ttc 352
Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe
                           75          80          85          90

aaa tgt agt gtg aaa ggc tct gga atc tcc agc tat gga aat aac ccc 400
Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro
                           95          100          105

caa gat gtc ccc aga gcc ttt gag gag tgt atg caa aaa gtc aag ggg 448
Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly
                           110         115         120

cag gtt cca tcc cac ctc cac gga tcc acc ccc att cac ctg gga gcc 496
Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala
                           125         130         135

acg gct ggg atg cgc ttg ctg agg ttg caa aat gaa aca gca gct aat 544
Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn
                           140         145         150

gaa gtc ctt gaa agc atc caa agc tac ttc aag tcc cag ccc ttt gac 592
Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp
                           155         160         165         170

```

ttt agg ggt gct caa atc att tct ggg caa gaa gaa ggg gta tat gga	640
Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly	
175 180 185	
tgg att aca gcc aac tat tta atg gga aat ttc ctg gag aag aac ctg	688
Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu	
190 195 200	
tgg cac atg tgg gtc cac ccg cat gga gtc gaa acc acg ggt gcc ctg	736
Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu	
205 210 215	
gac tta ggt ggt gcc tcc acc caa ata tcc ttc gtc gca gga gag aag	784
Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys	
220 225 230	
atg gat ctg aac acc agc gac atc atg cag gtc tcc ctg tat ggc tac	832
Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr	
235 240 245 250	
gta tac acg ctc tac aca cac agc ttc cag tgc tat ggc cgg aat gag	880
Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu	
255 260 265	
gct gag aag ttt ctg gca atg ctc ctg cag aat tct cct acc aaa	928
Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys	
270 275 280	
aac cat ctc acc aat ccc tgt tac cct cgg gat tat agc atc agc ttc	976
Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe	
285 290 295	
acc atg ggc cat gta ttt gat agc ctg tgc act gtc gac cag agg cca	1024
Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro	
300 305 310	
gaa agt tat aac ccc aat gat gtc atc act ttt gaa gga act ggg gac	1072
Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp	
315 320 325 330	
cca tct ctg tgt aag gag aag gtc gct tcc ata ttt gac ttc aaa gct	1120
Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala	
335 340 345	
tgc cat gat caa gaa acc tgt tct ttt gat ggg gtt tat cag cca aag	1168
Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys	
350 355 360	
att aaa ggg cca ttt gtc gct ttt gca gga ttc tac tac aca gcc agt	1216
Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser	
365 370 375	
gct tta aat ctt tca ggt agc ttt tcc ctg gac acc ttc aac tcc agc	1264
Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser	
380 385 390	

acc tgg aat ttc tgc tca cag aat tgg agt cag ctc cca ctg ctg ctc Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu 395 400 405 410	1312
ccc aaa ttt gat gag gta tat gcc cgc tct tac tgc ttc tca gcc aac Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn 415 420 425	1360
tac atc tac cac ttq ttt gtg aac ggt tac aaa ttc aca gag gag act Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr 430 435 440	1408
tgg ccc caa ata cac ttt gaa aaa gaa gtg ggg aat agc agc ata gcc Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala 445 450 455	1456
tgg tct ctt ggc tac atg ctc agc ctg acc aac cag atc cca gct gaa Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu 460 465 470	1504
agc cct ctg atc cgt ctg ccc ata gaa cca cct gtc ttt gtg ggc acc Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr 475 480 485 490	1552
ctc gct ttc ttc aca gtg gca gcc ttg ctg tgt ctg gca ttt ctt gca Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala 495 500 505	1600
tac ctg tgt tca gca acc aga aga aag agg cac tcc gag cat gcc ttt Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe 510 515 520	1648
gac cat gca gtg gat tct gac tgagccttca aagcagctcc tggagtccaa Asp His Ala Val Asp Ser Asp 525	1699
tggctgctta gagtcagcct ggggtggcacc aggcaatgca ggtgaagtgg ctgccttcag 1759	
gaaataacaac taactaaaat caaacaccta ggtcacgtgc ctctcaaata ctgatttctg 1819	
ccacagcacc tcttgaggca tcccttggct attctgtgca tattgttctt cagagacctc 1879	
actacccaca tgctgatcta ttgggaaaca gagaagagac aggccactaa ggtcaggctc 1939	
tttatattaa gttccccaga ggaagagtaa gttgagaagg tatcagttt atgttgaaga 1999	
attgacctca gggctcagtt tccatttccc tccctcagta ttcttcctgg caagataccc 2059	
attnaaggatt tcgccaatca gaatctcatt ttatagttt tcccatgggt ctttaactaa 2119	
gactttcttg tagcaatctc gtaagcagtg aacccctca gatcagtaga atatagtatc 2179	
tgggggagaa gacttacttc cttagggca gcagccacag ccaggttct gtcatacagg 2239	
tagatcccga agcacagaga cataaaaaag gtctcccaga aaactataga ccattctcca 2299	
agtggaaattc ccacttaggg ctctggcac tagattgcaa cctgtgttt tgcatacatc 2359	

ctcatctcac cattgttattg ctatgccctc ccataaaaac acattgatcc ctagcaagat 2419
tattgcattc cagattttac tgccttgct aggctttgc ttagcaaagg gctgactttc 2479
cattgttatac atgggtgtata tattttgtc accattccca caagtatact tgatgttgtc 2539
atagaacgaa catcctactc tatgatttac taaccaatta ctttcccaga tcatagacct 2599
ctctgcatacg tagtcatagg tcttgacttt ggggaaagaa aaggaagctg caggaatatt 2659
tatctccaaa gtcgaatgag aaagaactcc agcaaatcca atggctacaa actaaaaatc 2719
agcattattt catattgctg tttcttagct gaatatggaa taaagaacta ttatttatt 2779
ttgaaaaaaaa aaaaaaaaaa 2797

<210> 4
<211> 529
<212> PRT
<213> Homo sapiens

<400> 4
Met Phe Thr Val Leu Thr Arg Gln Pro Cys Glu Gln Ala Gly Leu Lys
1 5 10 15
Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala Leu Val Val Leu Leu Val
20 25 30
Ser Ile Val Val Leu Val Ser Ile Thr Val Ile Gln Ile His Lys Gln
35 40 45
Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly Ile Val Leu Asp Ala Gly
50 55 60
Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln Trp Pro Ala Glu Lys Glu
65 70 75 80
Asn Asn Thr Gly Val Val Ser Gln Thr Phe Lys Cys Ser Val Lys Gly
85 90 95
Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro Gln Asp Val Pro Arg Ala
100 105 110
Phe Glu Glu Cys Met Gln Lys Val Lys Gly Gln Val Pro Ser His Leu
115 120 125
His Gly Ser Thr Pro Ile His Leu Gly Ala Thr Ala Gly Met Arg Leu
130 135 140
Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn Glu Val Leu Glu Ser Ile
145 150 155 160
Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp Phe Arg Gly Ala Gln Ile
165 170 175
Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly Trp Ile Thr Ala Asn Tyr
180 185 190

Leu Met Gly Asn Phe Leu Glu Lys Asn Leu Trp His Met Trp Val His
195 200 205

Pro His Gly Val Glu Thr Thr Gly Ala Leu Asp Leu Gly Gly Ala Ser
210 215 220

Thr Gln Ile Ser Phe Val Ala Gly Glu Lys Met Asp Leu Asn Thr Ser
225 230 235 240

Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr Val Tyr Thr Leu Tyr Thr
245 250 255

His Ser Phe Gln Cys Tyr Gly Arg Asn Glu Ala Glu Lys Lys Phe Leu
260 265 270

Ala Met Leu Leu Gln Asn Ser Pro Thr Lys Asn His Leu Thr Asn Pro
275 280 285

Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe Thr Met Gly His Val Phe
290 295 300

Asp Ser Leu Cys Thr Val Asp Gln Arg Pro Glu Ser Tyr Asn Pro Asn
305 310 315 320

Asp Val Ile Thr Phe Glu Gly Thr Gly Asp Pro Ser Leu Cys Lys Glu
325 330 335

Lys Val Ala Ser Ile Phe Asp Phe Lys Ala Cys His Asp Gln Glu Thr
340 345 350

Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys Ile Lys Gly Pro Phe Val
355 360 365

Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser Ala Leu Asn Leu Ser Gly
370 375 380

Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser Thr Trp Asn Phe Cys Ser
385 390 395 400

Gln Asn Trp Ser Gln Leu Pro Leu Leu Pro Lys Phe Asp Glu Val
405 410 415

Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn Tyr Ile Tyr His Leu Phe
420 425 430

Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr Trp Pro Gln Ile His Phe
435 440 445

Glu Lys Glu Val Gly Asn Ser Ser Ile Ala Trp Ser Leu Gly Tyr Met
450 455 460

Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu Ser Pro Leu Ile Arg Leu
465 470 475 480

Pro Ile Glu Pro Pro Val Phe Val Gly Thr Leu Ala Phe Phe Thr Val
485 490 495

Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala Tyr Leu Cys Ser Ala Thr
500 505 510

Arg Arg Lys Arg His Ser Glu His Ala Phe Asp His Ala Val Asp Ser
515 520 525

Asp

<210> 5
<211> 1998
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (247)..(1530)

<400> 5
gcgcgcgcgt tttccttgtt cctggtaaac aaagaaatgt ggagtgtctt ggctgaatcc 60
tcatacagac aagatcatta tggtgctgtt aggtaggact tgtatccaga tgtaaggttg 120
aaaaagtgtat ataataaagg aaccaaggag aaaattcaga aggaaagaaa aaattgcctc 180
tgcaggtgtg cgagcaggat tgcttctgca acaaaagcct ccaccagcc acatcttggg 240
aaaaga atg gcc act tct tgg ggc aca gtc ttt ttc atg ctg gtg gta 288
Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val
1 5 10

tcc tgt gtt tgc agc gct gtc tcc cac agg aac cag cag act tgg ttt 336
Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe
15 20 25 30

gag ggt atc ttc ctg tct tcc atg tgc ccc atc aat gtc agc gcc agc 384
Glu Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser
35 40 45

acc ttg tat gga att atg ttt gat gca ggg agc act gga act cga att 432
Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile
50 55 60

cat gtt tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta 480
His Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu
65 70 75

gaa ggg gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta 528
Glu Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val
80 85 90

gat caa cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg 576
Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val
95 100 105 110

gcc aaa gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc Ala Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val 115 120 125	624
cta aag gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys 130 135 140	672
gct ctg ctc ttt gag gta aag qaq atc ttc agg aag tca cct ttc ctg Ala Leu Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu 145 150 155	720
gta cca aag ggc agt gtt agc atc atg gat gga tcc gac gaa ggc ata Val Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile 160 165 170	768
tta gct tgg gtt act gtt aat ttt ctg aca ggt cag ctg cat ggc cac Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His 175 180 185 190	816
aga cag gag act gtt ggg acc ttg gac cta ggg gga gcc tcc acc caa Arg Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln 195 200 205	864
atc acg ttc ctg ccc cag ttt gag aaa act ctg gaa caa act cct agg Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg 210 215 220	912
ggc tac ctc act tcc ttt gag atg ttt aac agc act tat aag ctc tat Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr 225 230 235	960
aca cat agt tac ttg gga ttt gga ttg aaa gct gca aga cta gca acc Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr 240 245 250	1008
ctg gga gcc ctg gag aca gaa ggg act gat ggg cac act ttc cgg agt Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser 255 260 265 270	1056
gcc tgt tta ccg aga tgg ttg gaa gca gag tgg atc ttt ggg ggt gtg Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val 275 280 285	1104
aaa tac cag tat ggt ggc aac caa gaa ggg gag gtg ggc ttt gag ccc Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro 290 295 300	1152
tgc tat gcc gaa gtg ctg agg gtg gta cga gga aaa ctt cac cag cca Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro 305 310 315	1200
gag gag gtc cag aga ggt tcc ttc tat gct ttc tct tac tat tat gac Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp 320 325 330	1248

cga gct gtt gac aca gac atg att gat tat gaa aag ggg ggt att tta	1296
Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu	
335 340 345 350	
aaa gtt gaa gat ttt gaa aga aaa gcc agg gaa gtg tgt gat aac ttg	1344
Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu	
355 360 365	
gaa aac ttc acc tca ggc agt cct ttc ctg tgc atg gat ctc agc tac	1392
Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr	
370 375 380	
atc aca gcc ctg tta aag gat ggc ttt ggc ttt gca gac agc aca gtc	1440
Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val	
385 390 395	
tta cag ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg	1488
Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu	
400 405 410	
ggg gcc acc ttt cac ctg ttg cag tct ctg ggc atc tcc cat	1530
Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His	
415 420 425	
tgaggccacg tacttccttg gagacctgca tttgccaaca ccttttaag gggaggagag	1590
agcacttagt ttctgaacta gtctggaca tcctggactt gagcctagag atttaggttt	1650
aattaatttt acacatctaa tgtgaactgc tgccaaacca ctcaagagta cacagctggc	1710
accagagcat cacagagagc cctgtgagcc aaaaagtata gttttggaac ttaaccttgg	1770
agtgagagcc cagggacagg tccctggaaa ccaaagaaaa atcgatttc aaccctttga	1830
gtgcctcatt ccactgaata tttaaatttt cctcttaaat ggtaaactga cttattgcaa	1890
tcccaagacc catcaatatac agtattttt tcctccctat acagtccct gcccaccctt	1950
atctgcaccc acctccccctg aaaaagagag aaaaaaaaaa aaaaaaaaaa	1998

<210> 6
 <211> 428
 <212> PRT
 <213> Homo sapiens

<400> 6	
Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys	
1 5 10 15	
Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly	
20 25 30	
Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu	
35 40 45	
Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val	
50 55 60	

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
 65 70 75 80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
 85 90 95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
 100 105 110

Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
 115 120 125

Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
 130 135 140

Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
 145 150 155 160

Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
 165 170 175

Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
 180 185 190

Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
 195 200 205

Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
 210 215 220

Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
 225 230 235 240

Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
 245 250 255

Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
 260 265 270

Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
 275 280 285

Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
 290 295 300

Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
 305 310 315 320

Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
 325 330 335

Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
 340 345 350

Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
 355 360 365

Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
370 375 380

Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385 390 395 400

Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
405 410 415

Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
420 425

<210> 7

<211> 2119

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (205)..(1599)

<400> 7

acgttgacac aggaatgaag agtgtattgg ctgaatcttc aagcagaggc gatattgacc 60

atgtgcttt taaattggcc tgcgtgaccc gcccacttgg tgtaaaagaa gaaccggcca 120

aagggagggc ctgaaggacc tccacaggag tgtgagcagc actgcttcag caacaaagcc 180

tcaggtccac atcttggaa gaat atg gcc act tcc tgg ggg gct gtc ttc 231
Met Ala Thr Ser Trp Gly Ala Val Phe
1 5

atg ctg atc ata gcc tgc gtt ggc agc act gtc ttc tac aga gaa cag 279
Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln
10 15 20 25

cag acc tgg ttt gaa ggt gtc ttc ttg tct tcc atg tgc ccc att aat 327
Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn
30 35 40

gtc agt gcc ggc acc ttt tat gga att atg ttt gat gcg ggc agc act 375
Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
45 50 55

gga gct cgg att cat gtt tac act ttt gtg cag aaa aca gca gga cag 423
Gly Ala Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln
60 65 70

ctc ccc ttt ctg gaa ggt gaa att ttt gat tct gtg aag ccg gga ctt 471
Leu Pro Phe Leu Glu Gly Glu Ile Phe Asp Ser Val Lys Pro Gly Leu
75 80 85

tct gct ttt gtg gat cag ccc aaa cag ggt gct gag act gtc cag gag 519
Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu
90 95 100 105

ctc ttg gag gtg gcc aaa gac tcg atc ccc aga agc cac tgg gaa agg	567
Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg	
110 115 120	
acc ccg gtg gtt ctg aaa gca acg gcc gga ctc cgt ttg ctg cct gag	615
Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu	
125 130 135	
cag aaa gcc caq gct ctg ctc ttg gag gta gag gag atc ttc aag aat	663
Gln Lys Ala Gln Ala Leu Leu Leu Glu Val Glu Glu Ile Phe Lys Asn	
140 145 150	
tca cct ttc ctg gtc cca gat ggc agc gtt agc atc atg gat ggg tcc	711
Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser	
155 160 165	
tat gaa ggc ata cta gcc tgg gtt acc gtg aac ttt cta aca ggt cag	759
Tyr Glu Gly Ile Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln	
170 175 180 185	
ctg cat ggt cgt ggc cag gag act gtg ggg acc ctt gac ctg ggg ggt	807
Leu His Gly Arg Gly Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly	
190 195 200	
gcc tcc acc caa atc acg ttt cta ccc cag ttt gag aaa acc ctg gaa	855
Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu	
205 210 215	
caa aca cct agg ggc tac ctc act tcc ttt gag atg ttt aac agc act	903
Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr	
220 225 230	
ttt aag ctc tat aca cat agt tac ttg gga ttt gga ctg aaa gct gca	951
Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala	
235 240 245	
aga ctg gca act ctg gga gcc ctg gaa gca aaa ggg act gat gga cat	999
Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His	
250 255 260 265	
acg ttt cga agt gcc tgt tta cca aga tgg ttg gaa gca gag tgg atc	1047
Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile	
270 275 280	
ttt ggg ggt gtg aaa tac cag tat ggt ggt aac caa gaa ggg gag atg	1095
Phe Gly Gly Val Lys Tyr Gin Tyr Gly Gly Asn Gln Glu Gly Glu Met	
285 290 295	
ggc ttt gaa ccc tgc tat gcg gaa gtg ctg agg gta gta cag ggg aaa	1143
Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys	
300 305 310	
ctt cac cag cca gaa gaa gtc cga gga agc gcc ttc tac gct ttc tct	1191
Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser	
315 320 325	

tac tac tac gat cga gcc gct gac aca cac ttg atc gat tat gaa aag		1239
Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys		
330 335 340 345		
ggc ggg gtt tta aaa gtt gaa gat ttt gaa aga aaa gcc aga gaa gtg		1287
Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val		
350 355 360		
tgt gac aac ttg ggg agc ttc tcc tcg ggc agt cct ttc ctc tgc atg		1335
Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met		
365 370 375		
gac ctc act tac atc aca gcc ctg ttg aaa gat ggt ttg ggc ttt gcc		1383
Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala		
380 385 390		
gaa cgg cac cct ctt aca gct cac aaa gaa agt gaa caa cat aga gac		1431
Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp		
395 400 405		
tgg ttg ggc ctt ggg ggc cac ctt tca cct gct cca gtc tct ggg cat		1479
Trp Leu Gly Leu Gly His Leu Ser Pro Ala Pro Val Ser Gly His		
410 415 420 425		
cac cag ctg agg cca agc tcc acc tct gaa gcc tgc att tct gaa cca		1527
His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro		
430 435 440		
gtt ttc tca cag gaa ggc gtg gac tca gag aca ttt tct gac ctc tct		1575
Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser		
445 450 455		
gga aaa gcc tgg ccc gaa acc cgt taactggttt tataaggagg gaggggtttt		1629
Gly Lys Ala Trp Pro Glu Thr Arg		
460 465		
tagatgagtc ttgctcttga gcctagtat ttgggcttca atgatttgc catctaatgt		1689
gaatagctcc taaccacttg gtgggtgcat ggctggcacc agactgtaaa tctttggga		1749
ttctttgtac agagtccctgc aaaggaaaaa agagaaaagg tttggaaactc catgctagat		1809
tgcgagttca gagacaggtc cctggggacc aaagaacaat ctcgtttcaa cccttggatg		1869
cctcattgct ttgaatggat tcattttgc ttataagctg atttactgaa atcccataac		1929
ccatcaatgc tgttaatttt ttcttccta cccttattac attcccttacc ctaaaagcct		1989
ggggaaataa cctgggtttt cttccatct ataattgaga aagagggggg aaaagatact		2049
gtattagaat ttgtgtgatc ctgtggcaca atagatcaac caaccatc aaagcttaaa		2109
aaaaaaaaaa		2119

<210> 8
 <211> 465
 <212> PRT

<213> **Mus musculus**

<400> 8
Met Ala Thr Ser Trp Gly Ala Val Phe Met Leu Ile Ile Ala Cys Val
1 5 10 15
Gly Ser Thr Val Phe Tyr Arg Glu Gln Gln Thr Trp Phe Glu Gly Val
20 25 30
Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Gly Thr Phe Tyr
35 40 45
Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Ala Arg Ile His Val Tyr
50 55 60
Thr Phe Val Gln Lys Thr Ala Gly Gln Leu Pro Phe Leu Glu Gly Glu
65 70 75 80
Ile Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln Pro
85 90 95
Lys Gln Gly Ala Glu Thr Val Gln Glu Leu Leu Glu Val Ala Lys Asp
100 105 110
Ser Ile Pro Arg Ser His Trp Glu Arg Thr Pro Val Val Leu Lys Ala
115 120 125
Thr Ala Gly Leu Arg Leu Leu Pro Glu Gln Lys Ala Gln Ala Leu Leu
130 135 140
Leu Glu Val Glu Glu Ile Phe Lys Asn Ser Pro Phe Leu Val Pro Asp
145 150 155 160
Gly Ser Val Ser Ile Met Asp Gly Ser Tyr Glu Gly Ile Leu Ala Trp
165 170 175
Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly Arg Gly Gln Glu
180 185 190
Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr Phe
195 200 205
Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr Leu
210 215 220
Thr Ser Phe Glu Met Phe Asn Ser Thr Phe Lys Leu Tyr Thr His Ser
225 230 235 240
Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly Ala
245 250 255
Leu Glu Ala Lys Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys Leu
260 265 270
Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr Gln
275 280 285

Tyr Gly Gly Asn Gln Glu Gly Glu Met Gly Phe Glu Pro Cys Tyr Ala
 290 295 300
 Glu Val Leu Arg Val Val Gln Gly Lys Leu His Gln Pro Glu Glu Val
 305 310 315 320
 Arg Gly Ser Ala Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala Ala
 325 330 335
 Asp Thr His Leu Ile Asp Tyr Glu Lys Gly Gly Val Leu Lys Val Glu
 340 345 350
 Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Gly Ser Phe
 355 360 365
 Ser Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Thr Tyr Ile Thr Ala
 370 375 380
 Leu Leu Lys Asp Gly Leu Gly Phe Ala Glu Arg His Pro Leu Thr Ala
 385 390 395 400
 His Lys Glu Ser Glu Gln His Arg Asp Trp Leu Gly Leu Gly Gly His
 405 410 415
 Leu Ser Pro Ala Pro Val Ser Gly His His Gln Leu Arg Pro Ser Ser
 420 425 430
 Thr Ser Glu Ala Cys Ile Ser Glu Pro Val Phe Ser Gln Glu Gly Val
 435 440 445
 Asp Ser Glu Thr Phe Ser Asp Leu Ser Gly Lys Ala Trp Pro Glu Thr
 450 455 460
 Arg
 465

 <210> 9
 <211> 428
 <212> PRT
 <213> Homo sapiens

 <400> 9
 Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
 1 5 10 15
 Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
 20 25 30
 Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
 35 40 45
 Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
 50 55 60
 Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
 65 70 75 80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
 85 90 95

 Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
 100 105 110

 Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
 115 120 125

 Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
 130 135 140

 Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
 145 150 155 160

 Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
 165 170 175

 Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
 180 185 190

 Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
 195 200 205

 Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
 210 215 220

 Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
 225 230 235 240

 Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
 245 250 255

 Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
 260 265 270

 Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
 275 280 285

 Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
 290 295 300

 Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
 305 310 315 320

 Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
 325 330 335

 Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
 340 345 350

 Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
 355 360 365

 Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
 370 375 380

Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385 390 395 400

Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
405 410 415

Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
420 425

<210> 10
<211> 455
<212> PRT
<213> P. sativum

<400> 10
Met Glu Leu Leu Ile Lys Leu Ile Thr Phe Leu Leu Phe Ser Met Pro
1 5 10 15

Ala Ile Thr Ser Ser Gln Tyr Leu Gly Asn Asn Leu Leu Thr Ser Arg
20 25 30

Lys Ile Phe Leu Lys Gln Glu Glu Ile Ser Ser Tyr Ala Val Val Phe
35 40 45

Asp Ala Gly Ser Thr Gly Ser Arg Ile His Val Tyr His Phe Asn Gln
50 55 60

Asn Leu Asp Leu Leu His Ile Gly Lys Gly Val Glu Tyr Tyr Asn Lys
65 70 75 80

Ile Thr Pro Gly Leu Ser Ser Tyr Ala Asn Asn Pro Glu Gln Ala Ala
85 90 95

Lys Ser Leu Ile Pro Leu Leu Glu Gln Ala Glu Asp Val Val Pro Asp
100 105 110

Asp Leu Gln Pro Lys Thr Pro Val Arg Leu Gly Ala Thr Ala Gly Leu
115 120 125

Arg Leu Leu Asn Gly Asp Ala Ser Glu Lys Ile Leu Gln Ser Val Arg
130 135 140

Asp Met Leu Ser Asn Arg Ser Thr Phe Asn Val Gln Pro Asp Ala Val
145 150 155 160

Ser Ile Ile Asp Gly Thr Gln Glu Gly Ser Tyr Leu Trp Val Thr Val
165 170 175

Asn Tyr Ala Leu Gly Asn Leu Gly Lys Lys Tyr Thr Lys Thr Val Gly
180 185 190

Val Ile Asp Leu Gly Gly Ser Val Gln Met Ala Tyr Ala Val Ser
195 200 205

Lys Lys Thr Ala Lys Asn Ala Pro Lys Val Ala Asp Gly Asp Asp Pro
210 215 220

Tyr Ile Lys Lys Val Val Leu Lys Gly Ile Pro Tyr Asp Leu Tyr Val
 225 230 235 240
 His Ser Tyr Leu His Phe Gly Arg Glu Ala Ser Arg Ala Glu Ile Leu
 245 250 255
 Lys Leu Thr Pro Arg Ser Pro Asn Pro Cys Leu Leu Ala Gly Phe Asn
 260 265 270
 Gly Ile Tyr Thr Tyr Ser Gly Glu Glu Phe Lys Ala Thr Ala Tyr Thr
 275 280 285
 Ser Gly Ala Asn Phe Asn Lys Cys Lys Asn Thr Ile Arg Lys Ala Leu
 290 295 300
 Lys Leu Asn Tyr Pro Cys Pro Tyr Gln Asn Cys Thr Phe Gly Gly Ile
 305 310 315 320
 Trp Asn Gly Gly Gly Asn Gly Gln Lys Asn Leu Phe Ala Ser Ser
 325 330 335
 Ser Phe Phe Tyr Leu Pro Glu Asp Thr Gly Met Val Asp Ala Ser Thr
 340 345 350
 Pro Asn Phe Ile Leu Arg Pro Val Asp Ile Glu Thr Lys Ala Lys Glu
 355 360 365
 Ala Cys Ala Leu Asn Phe Glu Asp Ala Lys Ser Thr Tyr Pro Phe Leu
 370 375 380
 Asp Lys Lys Asn Val Ala Ser Tyr Val Cys Met Asp Leu Ile Tyr Gln
 385 390 395 400
 Tyr Val Leu Leu Val Asp Gly Phe Gly Leu Asp Pro Leu Gln Lys Ile
 405 410 415
 Thr Ser Gly Lys Glu Ile Glu Tyr Gln Asp Ala Ile Val Glu Ala Ala
 420 425 430
 Trp Pro Leu Gly Asn Ala Val Glu Ala Ile Ser Ala Leu Pro Lys Phe
 435 440 445
 Glu Arg Leu Met Tyr Phe Val
 450 455

<210> 11
 <211> 454
 <212> PRT
 <213> Solanum tuberosum

<400> 11
 Met Leu Asn Gln Asn Ser His Phe Ile Phe Ile Ile Leu Ala Ile Phe
 1 5 10 15
 Leu Val Leu Pro Leu Ser Leu Leu Ser Lys Asn Val Asn Ala Gln Ile
 20 25 30

Pro Leu Arg Arg His Leu Leu Ser His Glu Ser Glu His Tyr Ala Val
35 40 45

Ile Phe Asp Ala Gly Ser Thr Gly Ser Arg Val His Val Phe Arg Phe
50 55 60

Asp Glu Lys Leu Gly Leu Leu Pro Ile Gly Asn Asn Ile Glu Tyr Phe
65 70 75 80

Met Ala Thr Glu Pro Gly Leu Ser Ser Tyr Ala Glu Asp Pro Lys Ala
85 90 95

Ala Ala Asn Ser Leu Glu Pro Leu Leu Asp Gly Ala Glu Gly Val Val
100 105 110

Pro Gln Glu Leu Gln Ser Glu Thr Pro Leu Glu Leu Gly Ala Thr Ala
115 120 125

Gly Leu Arg Met Leu Lys Gly Asp Ala Ala Glu Lys Ile Leu Gln Ala
130 135 140

Val Arg Asn Leu Val Lys Asn Gln Ser Thr Phe His Ser Lys Asp Gln
145 150 155 160

Trp Val Thr Ile Leu Asp Gly Thr Gln Glu Gly Ser Tyr Met Trp Ala
165 170 175

Ala Ile Asn Tyr Leu Leu Gly Asn Leu Gly Lys Asp Tyr Lys Ser Thr
180 185 190

Thr Ala Thr Ile Asp Leu Gly Gly Ser Val Gln Met Ala Tyr Ala
195 200 205

Ile Ser Asn Glu Gln Phe Ala Lys Ala Pro Gln Asn Glu Asp Gly Glu
210 215 220

Pro Tyr Val Gln Gln Lys His Leu Met Ser Lys Asp Tyr Asn Leu Tyr
225 230 235 240

Val His Ser Tyr Leu Asn Tyr Gly Gln Leu Ala Gly Arg Ala Glu Ile
245 250 255

Phe Lys Ala Ser Arg Asn Glu Ser Asn Pro Cys Ala Leu Glu Gly Cys
260 265 270

Asp Gly Tyr Tyr Ser Tyr Gly Gly Val Asp Tyr Lys Val Lys Ala Pro
275 280 285

Lys Lys Gly Ser Ser Trp Lys Arg Cys Arg Arg Leu Thr Arg His Ala
290 295 300

Leu Lys Ile Asn Ala Lys Cys Asn Ile Glu Glu Cys Thr Phe Asn Gly
305 310 315 320

Val Trp Asn Gly Gly Asp Gly Gln Lys Asn Ile His Ala Ser
325 330 335

Ser Phe Phe Tyr Asp Ile Gly Ala Gln Val Gly Ile Val Asp Thr Lys
 340 345 350
 Phe Pro Ser Ala Leu Ala Lys Pro Ile Gln Tyr Leu Asn Ala Ala Lys
 355 360 365
 Val Ala Cys Gln Thr Asn Val Ala Asp Ile Lys Ser Ile Phe Pro Lys
 370 375 380
 Thr Gln Asp Arg Asn Ile Pro Tyr Leu Cys Met Asp Leu Ile Tyr Glu
 385 390 395 400
 Tyr Thr Leu Leu Val Asp Gly Phe Gly Leu Asn Pro His Lys Glu Ile
 405 410 415
 Thr Val Ile His Asp Val Gln Tyr Lys Asn Tyr Leu Val Gly Ala Ala
 420 425 430
 Trp Pro Leu Gly Cys Ala Ile Asp Leu Val Ser Ser Thr Thr Asn Lys
 435 440 445
 Ile Arg Val Ala Ser Ser
 450

<210> 12
 <211> 473
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 12
 Lys Thr Pro Glu Asp Ile Ser Ile Ile Pro Val Asn Asp Glu Pro Gly
 1 5 10 15
 Tyr Leu Gln Asp Ser Lys Thr Glu Gln Asn Tyr Pro Glu Leu Ala Asp
 20 25 30
 Ala Val Lys Ser Gln Thr Ser Gln Thr Cys Ser Glu Glu His Lys Tyr
 35 40 45
 Val Ile Met Ile Asp Ala Gly Ser Thr Gly Ser Arg Val His Ile Tyr
 50 55 60
 Lys Phe Asp Val Cys Thr Ser Pro Pro Thr Leu Leu Asp Glu Lys Phe
 65 70 75 80
 Asp Met Leu Glu Pro Gly Leu Ser Ser Phe Asp Thr Asp Ser Val Gly
 85 90 95
 Ala Ala Asn Ser Leu Asp Pro Leu Leu Lys Val Ala Met Asn Tyr Val
 100 105 110
 Pro Ile Lys Ala Arg Ser Cys Thr Pro Val Ala Val Lys Ala Thr Ala
 115 120 125
 Gly Leu Arg Leu Leu Gly Asp Ala Lys Ser Ser Lys Ile Leu Ser Ala
 130 135 140

Val Arg Asp His Leu Glu Lys Asp Tyr Pro Phe Pro Val Val Glu Gly
145 150 155 160

Asp Gly Val Ser Ile Met Gly Gly Asp Glu Glu Gly Val Phe Ala Trp
165 170 175

Ile Thr Thr Asn Tyr Leu Leu Gly Asn Ile Gly Ala Asn Gly Pro Lys
180 185 190

Leu Pro Thr Ala Ala Val Phe Asp Leu Gly Gly Ser Thr Gln Ile
195 200 205

Val Glu Glu Pro Thr Phe Pro Ile Asn Glu Lys Met Val Asp Gly Glu
210 215 220

His Lys Phe Asp Leu Lys Phe Gly Asp Glu Asn Tyr Thr Leu Tyr Gln
225 230 235 240

Phe Ser His Leu Gly Tyr Gly Leu Lys Glu Gly Arg Asn Lys Val Asn
245 250 255

Ser Val Leu Val Glu Asn Ala Leu Lys Asp Lys Ile Leu Lys Gly Cys
260 265 270

Asn Thr Lys Thr His Cys Leu Ser Ser Pro Cys Leu Pro Pro Lys Val
275 280 285

Asn Ala Thr Asn Glu Lys Val Thr Leu Glu Ser Lys Glu Thr Tyr Thr
290 295 300

Ile Asp Phe Ile Gly Pro Asp Glu Pro Ser Gly Ala Gln Cys Arg Phe
305 310 315 320

Leu Thr Asp Glu Ile Leu Asn Lys Asp Ala Gln Cys Gln Ser Pro Pro
325 330 335

Cys Ser Phe Asn Gly Val His Gln Pro Ser Leu Val Arg Thr Phe Lys
340 345 350

Glu Ser Asn Asp Ile Tyr Ile Phe Ser Tyr Phe Tyr Asp Arg Thr Thr
355 360 365

Arg Pro Leu Gly Met Pro Leu Ser Phe Thr Leu Asn Glu Leu Asn Asp
370 375 380

Leu Ala Arg Ile Val Cys Lys Gly Glu Glu Thr Trp Asn Ser Val Phe
385 390 , 395 400

Ser Gly Ile Ala Gly Ser Leu Asp Glu Leu Glu Ser Asp Ser His Phe
405 410 415

Cys Leu Asp Leu Ser Phe Gln Val Ser Leu Leu His Thr Gly Tyr Asp
420 425 430

Ile Pro Leu Gln Arg Glu Leu Arg Thr Gly Lys Lys Ile Ala Asn Lys
435 440 445

Glu Ile Gly Trp Cys Leu Gly Ala Ser Leu Pro Leu Leu Lys Ala Asp
450 455 460

Asn Trp Lys Cys Lys Ile Gln Ser Ala
465 470

<210> 13
<211> 153
<212> PRT
<213> Homo sapiens

<400> 13
Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr
1 5 10 15

Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His
20 25 30

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val
35 40 45

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg
50 55 60

Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr
65 70 75 80

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu
85 90 95

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr
100 105 110

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly
115 120 125

Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln
130 135 140

Lys Thr Arg Trp Phe Ser Ile Val Pro
145 150

<210> 14
<211> 154
<212> PRT
<213> Rattus norvegicus

<400> 14
Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Asn Leu
1 5 10 15

Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
20 25 30

Gln Leu Leu Glu Glu Cys Gln Val Lys Gly Pro Gly Ile Ser Lys Tyr
35 40 45

Ala Gln Lys Thr Asp Glu Ile Ala Ala Tyr Leu Ala Glu Cys Met Lys
50 55 60

Met Ser Thr Glu Arg Ile Pro Ala Ser Lys Gln His Gln Thr Pro Val
65 70 75 80

Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Lys
85 90 95

Gln Ser Ala Asp Glu Val Leu Ala Ala Val Ser Arg Ser Leu Lys Ser
100 105 110

Tyr Pro Phe Asp Phe Gln Gly Ala Lys Ile Ile Thr Gly Gln Glu Glu
115 120 125

Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Arg Phe Thr
130 135 140

Gln Glu Gln Ser Trp Leu Asn Phe Ile Ser
145 150

<210> 15

<211> 153

<212> PRT

<213> Homo sapiens

<400> 15

Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Met Phe
1 5 10 15

Ile Tyr Lys Trp Pro Ala Asp Lys Glu Asn Asp Thr Gly Ile Val Gly
20 25 30

Gln His Ser Ser Cys Asp Val Pro Gly Gly Ile Ser Ser Tyr Ala
35 40 45

Asp Asn Pro Ser Gly Ala Ser Gln Ser Leu Val Gly Cys Leu Glu Gln
50 55 60

Ala Leu Gln Asp Val Pro Lys Glu Arg His Ala Gly Thr Pro Leu Tyr
65 70 75 80

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Asn Leu Thr Asn Pro Glu
85 90 95

Ala Ser Thr Ser Val Leu Met Ala Val Thr His Thr Leu Thr Gln Tyr
100 105 110

Pro Phe Asp Phe Arg Gly Ala Arg Ile Leu Ser Gly Gln Glu Glu Gly
115 120 125

Val Phe Gly Trp Val Thr Ala Asn Tyr Leu Leu Glu Asn Phe Ile Lys
130 135 140

Tyr Gly Trp Val Gly Arg Trp Phe Arg
145 150

<210> 16
<211> 150
<212> PRT
<213> Gallus gallus

<400> 16

Phe	Lys	Tyr	Gly	Ile	Val	Leu	Asp	Ala	Gly	Ser	Ser	His	Thr	Ala	Val
1				5					10				15		

Phe Ile Tyr Lys Trp Pro Ala Asp Lys Glu Asn Asp Thr Gly Val Val

	20				25					30					
--	----	--	--	--	----	--	--	--	--	----	--	--	--	--	--

Ser Glu His Ser Met Cys Asp Val Glu Gly Pro Gly Ile Ser Ser Tyr

	35				40				45						
--	----	--	--	--	----	--	--	--	----	--	--	--	--	--	--

Ser Ser Lys Pro Pro Ala Ala Gly Lys Ser Leu Glu His Cys Leu Ser

	50				55			60							
--	----	--	--	--	----	--	--	----	--	--	--	--	--	--	--

Gln Ala Met Arg Asp Val Pro Lys Glu Lys His Ala Asp Thr Pro Leu

	65				70			75		80					
--	----	--	--	--	----	--	--	----	--	----	--	--	--	--	--

Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Thr Ile Ala Asp Pro

	85				90			95							
--	----	--	--	--	----	--	--	----	--	--	--	--	--	--	--

Pro Ser Gln Thr Cys Leu Ser Ala Val Met Ala Thr Leu Lys Ser Tyr

	100				105			110							
--	-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--

Pro Phe Asp Phe Gly Gly Ala Lys Ile Leu Ser Gly Glu Glu Gly

	115				120			125							
--	-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--

Val Phe Gly Trp Ile Thr Ala Asn Tyr Leu Leu Glu Asn Phe Ile Lys

	130				135			140							
--	-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--

Arg Gly Trp Leu Gly Glu

	145				150										
--	-----	--	--	--	-----	--	--	--	--	--	--	--	--	--	--

<210> 17
<211> 148
<212> PRT
<213> Caenorhabditis elegans

<400> 17

Ile	Lys	Tyr	Gly	Val	Ile	Cys	Asp	Ala	Gly	Ser	Ser	Gly	Thr	Arg	Leu
1				5					10				15		

Phe Val Tyr Thr Leu Lys Pro Leu Ser Gly Gly Leu Thr Asn Ile Asp

	20				25				30						
--	----	--	--	--	----	--	--	--	----	--	--	--	--	--	--

Thr Leu Ile His Glu Ser Gly Pro Val Val Lys Lys Val Thr Pro Gly

	35				40				45						
--	----	--	--	--	----	--	--	--	----	--	--	--	--	--	--

Leu Ser Ser Phe Gly Asp Lys Pro Glu Gln Val Val Glu Tyr Leu Thr

	50				55			60							
--	----	--	--	--	----	--	--	----	--	--	--	--	--	--	--

Pro Leu Leu Arg Phe Ala Glu Glu His Ile Pro Tyr Glu Gln Leu Gly

	65				70			75		80					
--	----	--	--	--	----	--	--	----	--	----	--	--	--	--	--

Glu Thr Asp Leu Leu Ile Phe Ala Thr Ala Gly Met Arg Leu Leu Pro
85 90 95

Glu Ala Gln Lys Asp Ala Ile Ile Lys Asn Leu Gln Asn Gly Leu Lys
100 105 110

Ser Val Thr Ala Leu Arg Val Ser Asp Ser Asn Ile Arg Ile Ile Asp
115 120 125

Gly Ala Trp Glu Gly Ile Tyr Ser Trp Ile Ala Val Asn Tyr Ile Leu
130 135 140

Gly Arg Phe Asp
145

<210> 18
<211> 10
<212> RNA
<213> Mus musculus

<400> 18
aagaauaagg 10

<210> 19
<211> 10
<212> RNA
<213> Vertebrate

<400> 19
gccggccaagg 10

<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
ccagactgta aatcttttgg 20

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
agggaatgta ataagggtag 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 22
ctgcttgagt gacgtctctg 20

<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
cacatgaggt tcagtcgtg 20

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
gtgaagtggc tgccttcagg 20

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
cctttgactc gggactccag 20

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
gaactgctgc ctaaccactc 20

<210> 27
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
attgatgggt cttgggattg c

21

<210> 28
<211> 10
<212> RNA
<213> Homo sapiens

<400> 28
augugaauga

10

<210> 29
<211> 10
<212> RNA
<213> Homo sapiens

<400> 29
acaaggaua

10